```
=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 10:01:27 ON 10 FEB 2003
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FILE COVERS 1907 - 10 Feb 2003  VOL 138 ISS 7
FILE LAST UPDATED: 7 Feb 2003  (20030207/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


=>
=>

=> d stat que
L1             1 SEA FILE=REGISTRY ABB=ON  PLU=ON  PVLDLLRELLEELKQKLK/SQSP
L2             2 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1


=>
=>

=> d ibib abs hitrn l2 1-2

L2   ANSWER 1 OF 2  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         1999:233772  HCAPLUS
DOCUMENT NUMBER:          130:262129
TITLE:                    Apolipoprotein A-I .alpha.-helical peptide analogs as
                          agonists for treatment of dyslipidemias
INVENTOR(S):              Dasseux, Jean-Louis; Sekul, Renate; Buttner, Klaus;
                          Cornut, Isabelle; Metz, Gunther; Dufourcq, Jean
PATENT ASSIGNEE(S):       USA
SOURCE:                   PCT Int. Appl., 232 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

      PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
      ----------------  ----  --------      ---------------  --------
      WO 9916409         A2   19990408      WO 1998-US20329  19980928
          W:  AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
              DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG,
              KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,
              NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
              UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
          RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
              FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
              CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
```

CA 2304814	AA	19990408	CA 1998-2304814	19980928
EP 1039934	A1	20001004	EP 1998-950742	19980928
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
NO 2000001601	A	20000526	NO 2000-1601	20000328
PRIORITY APPLN. INFO.:			US 1997-940136 A	19970929
			WO 1998-US20329 W	19980928

OTHER SOURCE(S): MARPAT 130:262129

AB Analogs of the .alpha.-helical peptides of apolipoprotein A-I (ApoA-I) that can act as ApoA-I agonists or superagonists with many at least as active as wild-type ApoA-I are described for use in treatment of dyslipidemias. Genes for these peptides may be used in gene therapy (no data). Detail physicochem. requirements for the amphipathic .alpha.-helixes are given and these are quite different from the prior art understanding of the properties of amphipathic .alpha.-helixes of ApoA-I. A series of >250 amphipathic peptides were tested for their ability to activate LCAT. One of these peptides was found to stimulate the formation of HDL with incorporation of cholesterol.

IT **221884-94-2**
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(activation of LCAT by, as amphipathic .alpha.-helical ApoAI agonist; apolipoprotein A-I .alpha.-helical peptide analogs as agonists for treatment of dyslipidemias)

L2 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER:	1999:233771 HCAPLUS
DOCUMENT NUMBER:	130:262128
TITLE:	Apolipoprotein A-I agonists and their use to treat dyslipidemic disorders
INVENTOR(S):	Dasseux, Jean-Louis; Sekul, Renate; Buttner, Klaus; Cornut, Isabelle; Metz, Gunther
PATENT ASSIGNEE(S):	USA
SOURCE:	PCT Int. Appl., 245 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9916408	A2	19990408	WO 1998-US20328	19980928
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6037323	A	20000314	US 1997-940093	19970929
CA 2304931	AA	19990408	CA 1998-2304931	19980928
EP 1019010	A1	20000719	EP 1998-951979	19980928
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
AU 747823	B2	20020523	AU 1998-97791	19980928
US 6265377	B1	20010724	US 1999-465719	19991217
NO 2000001600	A	20000503	NO 2000-1600	20000328
US 2003008827	A1	20030109	US 2001-865989	20010525
PRIORITY APPLN. INFO.:			US 1997-940093 A	19970929
			WO 1998-US20328 W	19980928

OTHER SOURCE(S): MARPAT 130:262128

AB The present invention provides peptides and peptide analogs that mimic the structural and pharmacol. properties of human ApoA-I. The peptides and peptide analogs are useful to treat a variety of disorders assocd. with dyslipidemia.

IT **221884-94-2P**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PNU (Preparation, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(apolipoprotein A-I agonists and their use to treat dyslipidemic disorders)

=>
=>

=> fil reg
FILE 'REGISTRY' ENTERED AT 10:01:38 ON 10 FEB 2003
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Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 7 FEB 2003 HIGHEST RN 487578-67-6
DICTIONARY FILE UPDATES: 7 FEB 2003 HIGHEST RN 487578-67-6

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=> d .seq l1 1

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2003 ACS
RN 221884-94-2 REGISTRY
CN L-Lysinamide, 1-acetyl-L-prolyl-L-valyl-L-leucyl-L-.alpha.-aspartyl-L-leucyl-L-leucyl-L-arginyl-L-.alpha.-glutamyl-L-leucyl-L-leucyl-L-.alpha.-glutamyl-L-.alpha.-glutamyl-L-leucyl-L-lysyl-L-glutaminyl-L-lysyl-L-leucyl- (9CI) (CA INDEX NAME)
NTE modified

type	------ location ------		description
terminal mod.	Pro-1	-	N-acetyl
terminal mod.	Lys-18	-	C-terminal amide

SQL 18

SEQ 1 PVLDLLRELL EELKQKLK
========== ========
HITS AT: 1-18

REFERENCE 1: 130:262129

REFERENCE 2: 130:262128

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 09:49:05 ; Search time 29 Seconds
(without alignments)
127.891 Million cell updates/sec

Title: US-09-865-989-191
Perfect score: 85
Sequence: 1 PVLDLLRELLEELKQKLK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0 5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1 sp_archea:*
2 sp_bacteria:*
3 sp_fungi:*
4 sp_human:*
5 sp_invertebrate:*
6 sp_mammal:*
7 sp_mhc:*
8 sp_organelle:*
9 sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*

16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49.5	58.2	1156	17	Q8TK58	Q8tk58 methanosarc
2	49	57.6	182	16	Q9WXZ8	Q9wxz8 thermotoga
3	47	55.3	281	10	Q9FGU2	Q9fgu2 arabidopsis
4	47	55.3	658	5	Q9U3N1	Q9u3n1 caenorhabdi
5	46	54.1	383	17	Q8U0V9	Q8u0v9 pyrococcus
6	46	54.1	395	17	Q8U430	Q8u430 pyrococcus
7	46	54.1	413	5	Q25004	Q25004 homarus ame
8	45	52.9	277	16	Q92Q82	Q92q82 rhizobium m
9	45	52.9	341	16	Q9RVB3	Q9rvb3 deinococcus
10	45	52.9	447	16	Q8RD37	Q8rd37 thermoanaer
11	45	52.9	488	5	Q9U3E8	Q9u3e8 caenorhabdi
12	45	52.9	999	2	Q93JY2	Q93jy2 erwinia chr
13	44.5	52.4	84	17	Q8TYE1	Q8tye1 methanopyru
14	44	51.8	96	15	P89843	P89843 human immun
15	44	51.8	135	2	Q93IB0	Q93ib0 staphylococ
16	44	51.8	327	16	Q8R794	Q8r794 thermoanaer
17	44	51.8	334	16	Q9A8K6	Q9a8k6 caulobacter
18	44	51.8	343	2	P77840	P77840 chloroflexu
19	44	51.8	364	5	Q17983	Q17983 caenorhabdi
20	44	51.8	398	4	Q96KY5	Q96ky5 homo sapien
21	44	51.8	458	16	Q8R8N9	Q8r8n9 thermoanaer
22	44	51.8	487	16	Q98QF4	Q98qf4 mycoplasma
23	44	51.8	566	16	Q9PHU2	Q9phu2 campylobact
24	44	51.8	585	4	Q8WW52	Q8ww52 homo sapien
25	44	51.8	791	17	Q9YB89	Q9yb89 aeropyrum p
26	44	51.8	842	16	Q92FU6	Q92fu6 listeria in
27	44	51.8	842	16	Q8YAV6	Q8yav6 listeria mo
28	44	51.8	1078	5	Q18476	Q18476 caenorhabdi
29	44	51.8	1942	17	Q8TVI4	Q8tvi4 methanopyru
30	43.5	51.2	216	17	O58396	O58396 pyrococcus
31	43	50.6	199	15	Q9JCT2	Q9jct2 human immun
32	43	50.6	203	15	Q9JCX0	Q9jcx0 human immun
33	43	50.6	341	16	Q8YUZ2	Q8yuz2 anabaena sp

34	43	50.6	379	3	Q9P635	Q9p635 neurospora
35	43	50.6	383	17	Q9V0F0	Q9v0f0 pyrococcus
36	43	50.6	396	3	Q9USQ4	Q9usq4 schizosacch
37	43	50.6	398	17	O58030	O58030 pyrococcus
38	43	50.6	398	17	Q9UY32	Q9uy32 pyrococcus
39	43	50.6	405	2	Q04389	Q04389 bacillus sp
40	43	50.6	426	16	Q929T3	Q929t3 listeria in
41	43	50.6	462	12	Q9IBR4	Q9ibr4 spodoptera
42	43	50.6	469	16	Q8R8Q4	Q8r8q4 thermoanaer
43	43	50 6	522	12	Q9YVT0	Q9yvt0 melanoplus
44	43	50 6	571	17	Q980V7	Q980v7 sulfolobus
45	43	50 6	612	10	O65437	O65437 arabidopsis

ALIGNMENTS

RESULT 1
Q8TK58
ID Q8TK58 PRELIMINARY; PRT; 1156 AA.
AC Q8TK58;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phosphorylase.
GN MA3560.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;

RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011064; AAM06921.1; -.
KW Complete proteome.
SQ SEQUENCE 1156 AA; 130192 MW; 0280A362DC4BB5C6 CRC64;

Query Match 58.2%, Score 49.5; DB 17; Length 1156;
Best Local Similarity 57.9%, Pred. No. 1.7e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 1 PVLDL-LRELLEELKQKLK 18
|:|| |:|||||:::| |
Db 749 PILDRNLKELLEEIQKKAK 767

Search completed: February 10, 2003, 09:51:07
Job time : 32 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 09:49:05 ; Search time 11 Seconds
(without alignments)
67.870 Million cell updates/sec

Title: US-09-865-989-191
Perfect score: 85
Sequence: 1 PVLDLLRELLEELKQKLK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	57.6	378	1	2NPD_NEUCR	Q01284 neurospora
2	47	55.3	439	1	MYC_MARMO	P22555 marmota mon
3	47	55.3	785	1	PTA1_YEAST	Q01329 saccharomyc
4	47	55.3	833	1	GYRA_BACHD	O50628 bacillus ha
5	46	54.1	1453	1	Y373_BOVIN	Q9tu23 bos taurus

6	45	52.9	558	1	YCXA_ASTLO	P34782 astasia lon
7	44	51.8	134	1	YTKC_BACSU	O34883 bacillus su
8	44	51.8	433	1	APB_CHICK	P11682 gallus gall
9	43	50.6	420	1	DCDA_AQUAE	O67262 aquifex aeo
10	43	50.6	654	1	PGKT_THEMA	P36204 thermotoga
11	43	50.6	1075	1	Y124_METJA	Q57588 methanococc
12	43	50.6	1120	1	KEFA_ECOLI	P77338 escherichia
13	43	50.6	1166	1	ADDB_BACSU	P23477 bacillus su
14	43	50.6	1214	1	BRF1_HUMAN	P55201 homo sapien
15	42	49.4	106	1	YBC8_YEAST	P38202 saccharomyc
16	42	49.4	155	1	YF45_PSEAE	Q04628 pseudomonas
17	42	49.4	218	1	PURQ_METTH	O26270 methanobact
18	42	49.4	307	1	YJM6_YEAST	P47016 saccharomyc
19	42	49.4	315	1	RPOA_CLOAB	Q97ek6 clostridium
20	42	49.4	322	1	T121_ARCFU	O35003 archaeoglob
21	42	49.4	393	1	BM15_SHEEP	Q9mze2 ovis aries
22	42	49.4	437	1	MYC_FLVTT	P21438 feline leuk
23	42	49.4	438	1	MYC_CALJA	P49032 callithrix
24	42	49.4	439	1	MYC_CANFA	Q28350 canis famil
25	42	49.4	439	1	MYC_FELCA	P06877 felis silve
26	42	49.4	439	1	MYC_HUMAN	P01106 homo sapien
27	42	49.4	439	1	MYC_HYLLA	P49033 hylobates l
28	42	49.4	439	1	MYC_MOUSE	P01108 mus musculu
29	42	49.4	439	1	MYC_PANTR	P23583 pan troglod
30	42	49.4	439	1	MYC_RAT	P09416 rattus norv
31	42	49.4	457	1	SYS_SULSO	O33780 sulfolobus
32	42	49.4	621	1	TRA_STRLI	P22409 streptomyce
33	42	49 4	1088	1	RP17_MOUSE	Q99nf8 mus musculu
34	42	49 4	1539	1	Y373_HUMAN	O15078 homo sapien
35	41	48 2	150	1	TPC2_PONLE	P06708 pontastacus
36	41	48 2	226	1	VATE_BOVIN	P11019 bos taurus
37	41	48 2	226	1	VATE_HUMAN	P36543 homo sapien
38	41	48 2	226	1	YAI5_SCHPO	Q09893 schizosacch
39	41	48 2	228	1	VATE_MOUSE	P50518 mus musculu
40	41	48.2	263	1	MAZG_HAEIN	P44723 haemophilus
41	41	48 2	428	1	SYS_PASMU	P57836 pasteurella
42	41	48.2	441	1	VATH_ARATH	Q9lx65 arabidopsis
43	41	48.2	705	1	PPK_BACHD	Q9kd27 bacillus ha
44	41	48.2	884	1	SYA_RALSO	Q8y193 ralstonia s
45	41	48.2	1058	1	CARB_STRPN	Q97qe4 streptococc

ALIGNMENTS

RESULT 1
2NPD_NEUCR
ID 2NPD_NEUCR STANDARD; PRT; 378 AA.
AC Q01284;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 2-nitropropane dioxygenase precursor (EC 1.13.11.32) (Nitroalkane
DE oxidase) (2-NPD).
GN NCD-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=IFO 6067;
RX MEDLINE=98162064; PubMed=9501443;
RA Gorlatova N., Tchorzewski M., Kurihara T., Soda K., Esaki N.;
RT "Purification, characterization, and mechanism of a flavin
RT mononucleotide-dependent 2-nitropropane dioxygenase from Neurospora
RT crassa.";
RL Appl. Environ. Microbiol. 64:1029-1033(1998).
CC -!- FUNCTION: CATALYZES THE OXIDATION OF NITROALKANES TO PRODUCE
THE
CC CORRESPONDING CARBONYL COMPOUNDS. IT ACTS ON 2-NITROPROPANE
BETTER
CC THAN ON NITROETHANE AND 1-NITROPROPANE, AND ANIONIC FORMS OF
CC NITROALKANES ARE MUCH BETTER SUBSTRATES THAN ARE NEUTRAL
FORMS.
CC -!- CATALYTIC ACTIVITY: 2 2-nitropropane + O(2) = 2 acetone + 2
CC nitrite.
CC -!- COFACTOR: FMN.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: SOME, TO FAD-DEPENDENT 2-NITROPROPANE DIOXYGENASE.
CC ----------

CC ----------
DR EMBL; U22530; AAA64218.1; -.

DR InterPro; IPR004136; 2nprop_dioxygen.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF03060; NPD; 1.
KW Oxidoreductase; Dioxygenase; Flavoprotein; FMN.
FT PROPEP 1 15 POTENTIAL.
FT CHAIN 16 378 2-NITROPROPANE DIOXYGENASE.
SQ SEQUENCE 378 AA; 39916 MW; E453EB43FD23E441 CRC64;

Query Match 57.6%; Score 49; DB 1; Length 378;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
| |::||| || |:::|
Db 354 PAGDIVRELREEAKERIK 371
Search completed: February 10, 2003, 09:50:31
Job time : 14 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 09:49:05 ; Search time 15 Seconds
(without alignments)
115.361 Million cell updates/sec

Title: US-09-865-989-191
Perfect score: 85
Sequence: 1 PVLDLLRELLEELKQKLK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1 pir1 *
2 pir2 *
3 pir3 *
4 pir4:*

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	57.6	182	2	E72412	conserved hypothet

2	49	57.6	378	2	T46693	probable 2-nitropr
3	47	55.3	465	2	S03325	transforming prote
4	47	55.3	785	2	S31299	pre-tRNA processin
5	47	55.3	833	2	G83650	DNA gyrase subunit
6	47	55.3	833	2	T46552	DNA topoisomerase
7	46	54.1	322	1	W2WLE	E2 protein - human
8	45	52.9	341	2	C75436	hypothetical prote
9	45	52.9	558	2	S38614	hypothetical prote
10	44	51.8	134	2	D69994	autolytic amidase
11	44	51.8	334	2	D87416	delta-aminolevulin
12	44	51.8	364	2	T29709	probable aspartate
13	44	51.8	433	2	A29626	apolipoprotein B -
14	44	51.8	487	2	D90563	hypothetical prote
15	44	51.8	566	2	E81404	acetolactate synth
16	44	51.8	791	2	H72552	hypothetical prote
17	44	51.8	842	2	AH1432	DNA gyrase chain A
18	44	51.8	842	2	AH1433	DNA gyrase chain A
19	44	51.8	1078	2	T19745	hypothetical prote
20	43.5	51.2	216	2	H71111	hypothetical prote
21	43	50.6	341	2	AG2079	regulatory protein
22	43	50.6	383	2	H75129	probable transamin
23	43	50.6	396	2	T40559	hypothetical coile
24	43	50.6	398	2	F75017	probable glycine C
25	43	50.6	398	2	E71454	probable glycine C
26	43	50.6	405	2	T49534	hypothetical prote
27	43	50.6	420	1	C70404	diaminopimelate de
28	43	50.6	426	2	AD1706	weakly transcripti
29	43	50.6	522	2	T28323	ORF MSV162 probabl
30	43	50.6	571	2	D90157	hypothetical prote
31	43	50.6	612	2	T05331	hypothetical prote
32	43	50.6	654	2	G72344	phosphoglycerate k
33	43	50.6	1120	2	F90693	mechanosensitive c
34	43	50.6	1120	2	B85544	mechanosensitive c
35	43	50.6	1120	2	H64776	probable membrane
36	43	50.6	1163	2	D64315	type I restriction
37	43	50.6	1166	2	A39432	ATP-dependent deox
38	43	50.6	1214	2	JC2069	zinc-finger protei
39	43	50.6	1777	2	AC2088	serine/threonine k
40	42	49.4	97	2	D89792	conserved hypothet
41	42	49.4	106	2	S45762	hypothetical prote
42	42	49.4	155	2	H83453	hypothetical prote
43	42	49.4	156	2	AH0091	probable flagellar
44	42	49.4	186	2	I46085	proto-oncogene - c
45	42	49.4	218	2	E69091	phosphoribosylform

ALIGNMENTS

RESULT 1
E72412
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72412
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Nature 399, 323-329, 1999
A;Title Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of Thermotoga maritima.
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72412
A;Status: preliminary
A;Molecule type: DNA
A;Residues 1-182 <ARN>
A;Cross-references: GB:AE001700; GB:AE000512; NID:g4980636; PIDN:AAD35244.1; PID:g4980644; TIGR:TM0151
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0151

Query Match 57.6%; Score 49; DB 2; Length 182;
Best Local Similarity 61.1%; Pred. No. 20;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
||:| |:| ||| |||
Db 161 PVVDSRFEILAELKNKLK 178

Search completed: February 10, 2003, 09:50:13
Job time : 17 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 09:49:05 ; Search time 35 Seconds
(without alignments)
68.529 Million cell updates/sec

Title: US-09-865-989-191
Perfect score: 85
Sequence: 1 PVLDLLRELLEELKQKLK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	85	100.0	18	20	AAY19378	Lecithin:cholester
2	85	100.0	18	20	AAY19124	Lecithin:cholester
3	85	100.0	18	20	AAY18870	Lecithin:cholester
4	85	100.0	18	20	AAY18607	Lecithin:cholester
5	81	95.3	18	20	AAY19397	Lecithin:cholester
6	81	95.3	18	20	AAY19401	Lecithin:cholester
7	81	95.3	18	20	AAY19380	Lecithin cholester
8	81	95.3	18	20	AAY19143	Lecithin cholester
9	81	95.3	18	20	AAY19147	Lecithin cholester
10	81	95.3	18	20	AAY19126	Lecithin:cholester
11	81	95.3	18	20	AAY18893	Lecithin:cholester
12	81	95.3	18	20	AAY18889	Lecithin:cholester
13	81	95.3	18	20	AAY18872	Lecithin:cholester
14	81	95.3	18	20	AAY18626	Lecithin:cholester
15	81	95.3	18	20	AAY18630	Lecithin:cholester
16	81	95.3	18	20	AAY18609	Lecithin:cholester
17	78	91.8	18	20	AAY19394	Lecithin:cholester
18	78	91.8	18	20	AAY19379	Lecithin:cholester
19	78	91.8	18	20	AAY19384	Lecithin:cholester
20	78	91.8	18	20	AAY19130	Lecithin:cholester
21	78	91.8	18	20	AAY19140	Lecithin cholester
22	78	91.8	18	20	AAY19125	Lecithin cholester
23	78	91.8	18	20	AAY18876	Lecithin cholester
24	78	91.8	18	20	AAY18886	Lecithin cholester
25	78	91.8	18	20	AAY18871	Lecithin cholester
26	78	91.8	18	20	AAY18608	Lecithin:cholester
27	78	91.8	18	20	AAY18613	Lecithin:cholester

28	78	91.8	18	20	AAY18623	Lecithin:cholester
29	77	90.6	18	20	AAY19381	Lecithin:cholester
30	77	90.6	18	20	AAY19127	Lecithin:cholester
31	77	90.6	18	20	AAY19137	Lecithin:cholester
32	77	90.6	18	20	AAY18883	Lecithin:cholester
33	77	90.6	18	20	AAY18873	Lecithin:cholester
34	77	90.6	18	20	AAY18610	Lecithin:cholester
35	77	90.6	18	20	AAY18620	Lecithin:cholester
36	77	90.6	18	20	AAY19391	Lecithin:cholester
37	76	89.4	18	20	AAY19383	Lecithin:cholester
38	76	89.4	18	20	AAY19129	Lecithin:cholester
39	76	89.4	18	20	AAY18875	Lecithin:cholester
40	76	89.4	18	20	AAY18612	Lecithin:cholester
41	75	88.2	18	20	AAY19392	Lecithin:cholester
42	75	88.2	18	20	AAY19393	Lecithin:cholester
43	75	88.2	18	20	AAY19402	Lecithin:cholester
44	75	88.2	18	20	AAY19386	Lecithin:cholester
45	75	88.2	18	20	AAY19388	Lecithin:cholester

ALIGNMENTS

RESULT 1
AAY19378
ID AAY19378 standard; Peptide; 18 AA.
XX
AC AAY19378;
XX
DT 14-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #191.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916459-A1.
XX
PD 08-APR-1999.

XX
PF 28-SEP-1998; 98WO-US20327.
XX
PR 29-SEP-1997; 97US-0940095.
XX
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (DASS/) DASSEUX J.
PA (DUFO/) DUFOURCQ J
PA (METZ/) METZ G.
PA (SEKU/) SEKUL R.
XX
PI Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
PI Sekul R;
XX
DR WPI; 1999-277035/23.
XX
PT Peptide agonists of apolipoprotein A-I
XX
PS Example; Page 126; 280pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to
CC AAY19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 85; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
||||||||||||||||||
Db 1 PVLDLLRELLEELKQKLK 18

RESULT 2
AAY19124
ID AAY19124 standard; Peptide; 18 AA.
XX
AC AAY19124;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #191.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916458-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US20326.
XX
PR 29-SEP-1997; 97US-0940096.
XX
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (DASS/) DASSEUX J.
PA (METZ/) METZ G.
PA (SEKU/) SEKUL R.
XX
PI Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;
XX
DR WPI; 1999-277034/23.
XX
PT Peptide agonists of apolipoprotein A-I
XX
PS Example; Page 117; 254pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with

CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
CC AAY19187 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 85; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
||||||||||||||||||
Db 1 PVLDLLRELLEELKQKLK 18

RESULT 3
AAY18870
ID AAY18870 standard; Peptide; 18 AA.
XX
AC AAY18870;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #191.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916408-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US20328.

XX
PR 29-SEP-1997; 97US-0940093.
XX
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (DASS/) DASSEUX J.
PA (METZ/) METZ G.
PA (SEKU/) SEKUL R.
XX
PI Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;
XX
DR WPI; 1999-277031/23.
XX
PT Peptide agonists of apolipoprotein A-I
XX
PS Claim 15; Page 114; 152pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 14-22 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to
CC AAY18933 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 85; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
||||||||||||||||||
Db 1 PVLDLLRELLEELKQKLK 18

RESULT 4
AAY18607
ID AAY18607 standard; Peptide; 18 AA.

XX
AC AAY18607;
XX
DT 09-JUL-1999 (first entry)
XX
DE Lecithin cholesterol acyltransferase activation exhibiting peptide #191.
XX
KW Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9916409-A2.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US20329.
XX
PR 29-SEP-1997; 97US-0940136.
XX
PA (BUTT/) BUTTNER K.
PA (CORN/) CORNUT I.
PA (DASS/) DASSEUX J.
PA (DUFO/) DUFOURCQ J.
PA (METZ/) METZ G.
PA (SEKU/) SEKUL R.
XX
PI Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
PI Sekul R;
XX
DR WPI; 1999-254921/21.
XX
PT Nucleic acid encoding apolipoprotein A-I agonist peptides
XX
PS Claim 49; Page 182; 232pp; English.
XX
CC The present invention describes a nucleic acid (A) encoding an
CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
CC which forms an amphipathic alpha-helix in presence of lipids. (A),
CC optionally as a complex with lipids, and host cells that contain (A),
CC are useful for gene therapy, or prevention, of diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease,
CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I

CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
CC endotoxemia (septic shock). Host cells containing (A) can also be used
CC to study the role of apoA-I in lipid metabolism. (B) can be used
CC diagnostically, e.g. to measure serum HDL (particularly its
CC subpopulation involved in retrograde cholesterol transport) and for
CC imaging the circulatory system or HDL accumulations at fatty streaks.
CC The present sequence represents a peptide from the present invention.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 85; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18

Db 1 PVLDLLRELLEELKQKLK 18

Search completed: February 10, 2003, 09:49:49
Job time : 36 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 09:50:35 ; Search time 11 Seconds
(without alignments)
36.277 Million cell updates/sec

Title: US-09-865-989-191
Perfect score: 85
Sequence: 1 PVLDLLRELLEELKQKLK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	81	95 3	18	9	US-09-865-989-193	Sequence 193, App
3	81	95 3	18	9	US-09-865-989-210	Sequence 210, App
4	81	95 3	18	9	US-09-865-989-214	Sequence 214, App
5	78	91 8	18	9	US-09-865-989-192	Sequence 192, App
6	78	91 8	18	9	US-09-865-989-197	Sequence 197, App
7	78	91 8	18	9	US-09-865-989-207	Sequence 207, App
8	77	90 6	18	9	US-09-865-989-194	Sequence 194, App
9	77	90 6	18	9	US-09-865-989-204	Sequence 204, App
10	76	89.4	18	9	US-09-865-989-196	Sequence 196, App
11	75	88.2	18	9	US-09-865-989-199	Sequence 199, App
12	75	88.2	18	9	US-09-865-989-201	Sequence 201, App
13	75	88.2	18	9	US-09-865-989-205	Sequence 205, App
14	75	88.2	18	9	US-09-865-989-206	Sequence 206, App
15	75	88.2	18	9	US-09-865-989-215	Sequence 215, App
16	74	87.1	18	9	US-09-865-989-195	Sequence 195, App
17	74	87.1	18	9	US-09-865-989-198	Sequence 198, App
18	74	87.1	18	9	US-09-865-989-200	Sequence 200, App
19	74	87.1	18	9	US-09-865-989-203	Sequence 203, App
20	74	87.1	18	9	US-09-865-989-216	Sequence 216, App
21	74	87.1	18	9	US-09-865-989-221	Sequence 221, App
22	73	85.9	18	9	US-09-865-989-217	Sequence 217, App
23	73	85.9	18	9	US-09-865-989-220	Sequence 220, App
24	73	85.9	18	9	US-09-865-989-227	Sequence 227, App
25	73	85.9	18	9	US-09-865-989-228	Sequence 228, App
26	73	85.9	18	9	US-09-865-989-229	Sequence 229, App
27	73	85.9	18	9	US-09-865-989-231	Sequence 231, App
28	72	84.7	16	9	US-09-865-989-253	Sequence 253, App
29	71	83.5	18	9	US-09-865-989-232	Sequence 232, App
30	69	81.2	18	9	US-09-865-989-209	Sequence 209, App
31	69	81.2	18	9	US-09-865-989-218	Sequence 218, App
32	68	80.0	16	9	US-09-865-989-254	Sequence 254, App
33	68	80.0	18	9	US-09-865-989-219	Sequence 219, App
34	68	80.0	22	9	US-09-865-989-16	Sequence 16, Appl
35	67	78.8	16	9	US-09-865-989-258	Sequence 258, App
36	67	78.8	18	9	US-09-865-989-224	Sequence 224, App

37	67	78.8	22	9	US-09-865-989-130	Sequence 130, App
38	66	77.6	16	9	US-09-865-989-256	Sequence 256, App
39	65	76.5	22	9	US-09-865-989-39	Sequence 39, Appl
40	64	75.3	18	9	US-09-865-989-211	Sequence 211, App
41	64	75.3	22	9	US-09-865-989-1	Sequence 1, Appli
42	64	75.3	22	9	US-09-865-989-3	Sequence 3, Appli
43	64	75.3	22	9	US-09-865-989-4	Sequence 4, Appli
44	64	75.3	22	9	US-09-865-989-6	Sequence 6, Appli
45	64	75.3	22	9	US-09-865-989-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-865-989-191
; Sequence 191, Application US/09865989
; Publication No. US20030008827A1
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719

; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 191:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 18 amino acids
; TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
. MOLECULE TYPE: No. US20030008827A1e
, FEATURE:
, NAME/KEY: Other
, LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
, C-terminal amidated
; SEQUENCE DESCRIPTION: SEQ ID NO: 191:
US-09-865-989-191

Query Match 100.0%; Score 85; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
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Db 1 PVLDLLRELLEELKQKLK 18

Search completed: February 10, 2003, 09:54:37
Job time : 11 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: February 10, 2003, 09:49:05 ; Search time 14 Seconds
(without alignments)
37.829 Million cell updates/sec

Title: US-09-865-989-191
Perfect score: 85
Sequence: 1 PVLDLLRELLEELKQKLK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	85	100.0	18	3	US-08-940-095-191	Sequence 191, App
2	85	100.0	18	3	US-08-940-093-191	Sequence 191, App
3	85	100.0	18	3	US-08-940-096-191	Sequence 191, App
4	85	100.0	18	4	US-09-465-719-191	Sequence 191, App
5	85	100.0	18	4	US-09-453-605-191	Sequence 191, App
6	85	100.0	18	4	US-09-453-838-191	Sequence 191, App
7	81	95.3	18	3	US-08-940-095-193	Sequence 193, App
8	81	95.3	18	3	US-08-940-095-210	Sequence 210, App
9	81	95.3	18	3	US-08-940-095-214	Sequence 214, App
10	81	95.3	18	3	US-08-940-093-193	Sequence 193, App
11	81	95.3	18	3	US-08-940-093-210	Sequence 210, App
12	81	95 3	18	3	US-08-940-093-214	Sequence 214, App
13	81	95 3	18	3	US-08-940-096-193	Sequence 193, App
14	81	95 3	18	3	US-08-940-096-210	Sequence 210, App
15	81	95.3	18	3	US-08-940-096-214	Sequence 214, App
16	81	95 3	18	4	US-09-465-719-193	Sequence 193, App
17	81	95 3	18	4	US-09-465-719-210	Sequence 210, App
18	81	95 3	18	4	US-09-465-719-214	Sequence 214, App
19	81	95 3	18	4	US-09-453-605-193	Sequence 193, App
20	81	95 3	18	4	US-09-453-605-210	Sequence 210, App
21	81	95 3	18	4	US-09-453-605-214	Sequence 214, App
22	81	95 3	18	4	US-09-453-838-193	Sequence 193, App
23	81	95 3	18	4	US-09-453-838-210	Sequence 210, App
24	81	95 3	18	4	US-09-453-838-214	Sequence 214, App
25	78	91 8	18	3	US-08-940-095-192	Sequence 192, App
26	78	91 8	18	3	US-08-940-095-197	Sequence 197, App
27	78	91.8	18	3	US-08-940-095-207	Sequence 207, App
28	78	91.8	18	3	US-08-940-093-192	Sequence 192, App
29	78	91 8	18	3	US-08-940-093-197	Sequence 197, App
30	78	91 8	18	3	US-08-940-093-207	Sequence 207, App
31	78	91 8	18	3	US-08-940-096-192	Sequence 192, App
32	78	91 8	18	3	US-08-940-096-197	Sequence 197, App
33	78	91 8	18	3	US-08-940-096-207	Sequence 207, App
34	78	91 8	18	4	US-09-465-719-192	Sequence 192, App
35	78	91 8	18	4	US-09-465-719-197	Sequence 197, App
36	78	91 8	18	4	US-09-465-719-207	Sequence 207, App
37	78	91 8	18	4	US-09-453-605-192	Sequence 192, App
38	78	91 8	18	4	US-09-453-605-197	Sequence 197, App
39	78	91.8	18	4	US-09-453-605-207	Sequence 207, App
40	78	91.8	18	4	US-09-453-838-192	Sequence 192, App
41	78	91.8	18	4	US-09-453-838-197	Sequence 197, App
42	78	91.8	18	4	US-09-453-838-207	Sequence 207, App
43	77	90.6	18	3	US-08-940-095-194	Sequence 194, App
44	77	90.6	18	3	US-08-940-095-204	Sequence 204, App

ALIGNMENTS

RESULT 1
US-08-940-095-191
; Sequence 191, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT Sekul, Renate
; APPLICANT Buttner, Klaus
; APPLICANT Cornut, Isabelle
; APPLICANT Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION C-terminal amidated
US-08-940-095-191

Query Match 100.0%; Score 85; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
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Db 1 PVLDLLRELLEELKQKLK 18

RESULT 2
US-08-940-093-191
; Sequence 191, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; FEATURE
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
US-08-940-093-191

Query Match 100.0%; Score 85; DB 3; Length 18;
Best Local Similarity 100.0%; Pred No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
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Db 1 PVLDLLRELLEELKQKLK 18

RESULT 3
US-08-940-096-191

; Sequence 191, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE.
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e

; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
US-08-940-096-191

Query Match 100.0%, Score 85; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
||||||||||||||||||
Db 1 PVLDLLRELLEELKQKLK 18

RESULT 4
US-09-465-719-191
; Sequence 191, Application US/09465719
; Patent No 6265377
; GENERAL INFORMATION:
; APPLICANT Dasseux, Jean-Louis
; APPLICANT Sekul, Renate
; APPLICANT Buttner, Klaus
; APPLICANT Cornut, Isabelle
; APPLICANT Metz, Gunther
; TITLE OF INVENTION APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION N-terminal acetylated and
; OTHER INFORMATION C-terminal amidated
US-09-465-719-191

Query Match 100.0%; Score 85; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18
||||||||||||||||||
Db 1 PVLDLLRELLEELKQKLK 18

RESULT 5
US-09-453-605-191
; Sequence 191, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER US/09/453,605
; FILING DATE: 26-No. 6329341-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER 08/940,095
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; C-terminal amidated
; SEQUENCE DESCRIPTION: SEQ ID NO: 191:
US-09-453-605-191

Query Match 100.0%; Score 85; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18

Db 1 PVLDLLRELLEELKQKLK 18

RESULT 6
US-09-453-838-191
; Sequence 191, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...18
; OTHER INFORMATION: N-terminal acetylated and
; OTHER INFORMATION: C-terminal amidated
US-09-453-838-191

Query Match 100.0%; Score 85; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PVLDLLRELLEELKQKLK 18

Db 1 PVLDLLRELLEELKQKLK 18

Search completed: February 10, 2003, 09:51:26
Job time : 14 secs